



#4

Paper copy of sequence listing,
Pages 1 through 12
P-IU 3446
Serial No.: 09/438,917

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By Melanie K. Webster
Melanie K. Webster, Reg. No. 45,201

January 13, 2000
Date of Signature



- 1 -

SEQUENCE LISTING

<110> Welch, Peter J.
Barber, Jack R.

<120> Tumor Suppressor Molecules and Methods
of Use

<130> P-IU 3446

<140> US 09/438,917

<141> 1999-11-12

<160> 20

<170> FastSEQ for Windows Version 4.0

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<212> RNA

<213> Artificial Sequence

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<223> hairpin ribozyme

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<212> RNA

<213> homo sapiens

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<221> misc_feature

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<223> n = A,T,C or G

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Met Gly Gln Ser
1

ggg agg tcc cgg cac cag aag cgc gcc ccg ccc cag gcg cag ctc cgc 162
Gly Arg Ser Arg His Gln Lys Arg Ala Pro Pro Gln Ala Gln Leu Arg
5 10 15 20

aac ctc gag gcc tat gcc gcg aac ccg cac tcg ttc gtg ttc acg cga 210
Asn Leu Glu Ala Tyr Ala Ala Asn Pro His Ser Phe Val Phe Thr Arg
25 30 35

ggc tgc acg ggt cgc aac atc cgg cag ctc agc ctg gac gtg cgg cgg 258
Gly Cys Thr Gly Arg Asn Ile Arg Gln Leu Ser Leu Asp Val Arg Arg
40 45 50

gtc atg gag ccc gtc act gcc agc cgt ctg cag gtt cgt aag aag aac 306
Val Met Glu Pro Val Thr Ala Ser Arg Leu Gln Val Arg Lys Lys Asn
55 60 65

tcg ctg aag gac tgc gtg gca gtc gct ggg ccc ctc ggg gtc aca cac 354
Ser Leu Lys Asp Cys Val Ala Val Ala Gly Pro Leu Gly Val Thr His
70 75 80

ttt ctg atc cta gca aaa caa gag acc aat gtc tac ttt aag ctg atg 402
Phe Leu Ile Leu Ala Lys Gln Glu Thr Asn Val Tyr Phe Lys Leu Met
85 90 95 100

cgc ctc cca gga ggc ccc acc ttg acc ttc cag gtc aag aag tac tcg	450
Arg Leu Pro Gly Gly Pro Thr Leu Thr Phe Gln Val Lys Lys Tyr Ser	
105 110 115	
ctg gtg cgt gat gtg gtc tcc tca ctg cgc cgg cac cgc atg cac gag	498
Leu Val Arg Asp Val Val Ser Ser Leu Arg Arg His Arg Met His Glu	
120 125 130	
cag cag ttt gcc cac cca ccc ctc ctg gta ctc aac agc ttt ggc ccc	546
Gln Gln Phe Ala His Pro Pro Leu Leu Val Leu Asn Ser Phe Gly Pro	
135 140 145	
cat ggt atg cat gtg aag ctc atg gcc acc atg ttc cag aac ctg ttc	594
His Gly Met His Val Lys Leu Met Ala Thr Met Phe Gln Asn Leu Phe	
150 155 160	
ccc tcc atc aac gtg cac aag gtg aac ctg aac acc atc aag cgc tgc	642
Pro Ser Ile Asn Val His Lys Val Asn Leu Asn Thr Ile Lys Arg Cys	
165 170 175 180	
ctc ctc atc gac tac aac ccc gac tcc cag gag ctg gac ttc cgc cac	690
Leu Leu Ile Asp Tyr Asn Pro Asp Ser Gln Glu Leu Asp Phe Arg His	
185 190 195	
tat agc atc aaa gtt gtt cct gtg ggc gcg agt cgc ggg atg aag aag	738
Tyr Ser Ile Lys Val Val Pro Val Gly Ala Ser Arg Gly Met Lys Lys	
200 205 210	
ctg ctc cag gag aag ttc ccc aac atg agc cgc ctg cag gac atc agc	786
Leu Leu Gln Glu Lys Phe Pro Asn Met Ser Arg Leu Gln Asp Ile Ser	
215 220 225	
gag ctg ctg gcc acg ggc gcg ggg ctg tcg gag agc gag gca gag cct	834
Glu Leu Leu Ala Thr Gly Ala Gly Leu Ser Glu Ser Glu Ala Glu Pro	
230 235 240	
gac ggc gac cac aac atc aca gag ctg cct cag gct gtc gct ggc cgt	882
Asp Gly Asp His Asn Ile Thr Glu Leu Pro Gln Ala Val Ala Gly Arg	
245 250 255 260	
ggc aac atg cgg gcc cag cag agt gca gtg cgg ctc acc gag atc ggc	930
Gly Asn Met Arg Ala Gln Gln Ser Ala Val Arg Leu Thr Glu Ile Gly	
265 270 275	
ccg cgg atg aca ctg cag ctc atc aag gtc cag gag ggc gtc ggg gag	978
Pro Arg Met Thr Leu Gln Leu Ile Lys Val Gln Glu Gly Val Gly Glu	
280 285 290	
ggc aaa gtg atg ttc cac agt ttt gtg agc aag acg gag gag gag ctg	1026
Gly Lys Val Met Phe His Ser Phe Val Ser Lys Thr Glu Glu Glu Leu	
295 300 305	
cag gcc atc ctg gaa gcc aag gag aag aag ctg cgg ctg aag gct cag	1074

Gln Ala Ile Leu Glu Ala Lys Glu Lys Lys Leu Arg Leu Lys Ala Gln	
310 315 320	
agg cag gcc cag cag gcc cag aat gtg cag cgc aag cag gag cag cgg	1122
Arg Gln Ala Gln Gln Ala Gln Asn Val Gln Arg Lys Gln Glu Gln Arg	
325 330 335 340	
gag gcc cac aga aag aag agc ctg gag ggc atg aag aag gca cgg gtc	1170
Glu Ala His Arg Lys Lys Ser Leu Glu Gly Met Lys Lys Ala Arg Val	
345 350 355	
ggg ggt agt gat gaa gag gcc tct ggg atc cct tca agg acg gcg agc	1218
Gly Gly Ser Asp Glu Glu Ala Ser Gly Ile Pro Ser Arg Thr Ala Ser	
360 365 370	
ctg gag ttg ggt gag gac gat cat gaa cag gaa gat gat gac atc gag	1266
Leu Glu Leu Gly Glu Asp Asp His Glu Gln Glu Asp Asp Asp Ile Glu	
375 380 385	
tat ttc tgc cag gcg gtg ggc gag gcg ccc agt gag gac ctg ttc ccc	1314
Tyr Phe Cys Gln Ala Val Gly Glu Ala Pro Ser Glu Asp Leu Phe Pro	
390 395 400	
gag gcc aag cag aaa cgg ctt gcc aag tct cca ggg cgg aag cgg aag	1362
Glu Ala Lys Gln Lys Arg Leu Ala Lys Ser Pro Gly Arg Lys Arg Lys	
405 410 415 420	
cgg tgg gaa atg gat cga ggc agg ggt cgc ctt tgt gac cag aag ttt	1410
Arg Trp Glu Met Asp Arg Gly Arg Gly Arg Leu Cys Asp Gln Lys Phe	
425 430 435	
ccc aag aca aag gac aag tcc cag gga gcc cag gcc agg cgg ggg ccc	1458
Pro Lys Thr Lys Asp Lys Ser Gln Gly Ala Gln Ala Arg Arg Gly Pro	
440 445 450	
aga ggg gct tcc cgg gat ggt ggg cga ggc cgg ggc cga ggc cgc cca	1506
Arg Gly Ala Ser Arg Asp Gly Gly Arg Gly Arg Gly Arg Gly Arg Pro	
455 460 465	
ggg aag aga gtg gcc tga g cccaagccgc accggagcag cggctggatt	1555
Gly Lys Arg Val Ala *	
470	
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tccccagccc ttccactcca gtaaagaact gaattggcaa aaaaaaaaa	1664
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<212> PRT	
<213> homo sapiens	
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Val Phe Thr Arg	Gly Cys Thr Gly	Asn Ile Arg Gln	Leu Ser Leu
35	40	45	
Asp Val Arg Arg	Val Met Glu Pro Val Thr	Ala Ser Arg Leu	Gln Val
50	55	60	
Arg Lys Lys Asn	Ser Leu Lys Asp Cys Val	Ala Val Ala Gly	Pro Leu
65	70	75	80
Gly Val Thr His	Phe Leu Ile Leu Ala	Lys Gln Glu Thr	Asn Val Tyr
85	90	95	
Phe Lys Leu Met	Arg Leu Pro Gly Gly	Pro Thr Leu Thr	Phe Gln Val
100	105	110	
Lys Lys Tyr Ser	Leu Val Arg Asp Val	Val Ser Ser Leu	Arg Arg His
115	120	125	
Arg Met His Glu	Gln Gln Phe Ala His	Pro Pro Leu Leu	Val Leu Asn
130	135	140	
Ser Phe Gly Pro	His Gly Met His Val	Lys Leu Met Ala	Thr Met Phe
145	150	155	160
Gln Asn Leu Phe	Pro Ser Ile Asn Val	His Lys Val Asn	Leu Asn Thr
165	170	175	
Ile Lys Arg Cys	Leu Leu Ile Asp Tyr	Asn Pro Asp Ser	Gln Glu Leu
180	185	190	
Asp Phe Arg His	Tyr Ser Ile Lys Val	Val Pro Val Gly	Ala Ser Arg
195	200	205	
Gly Met Lys Lys	Leu Leu Gln Glu Lys	Phe Pro Asn Met	Ser Arg Leu
210	215	220	
Gln Asp Ile Ser	Glu Leu Leu Ala Thr	Gly Ala Gly Leu	Ser Glu Ser
225	230	235	240
Glu Ala Glu Pro	Asp Gly Asp His Asn	Ile Thr Glu Leu	Pro Gln Ala
245	250	255	
Val Ala Gly Arg	Gly Asn Met Arg Ala	Gln Gln Ser Ala	Val Arg Leu
260	265	270	
Thr Glu Ile Gly	Pro Arg Met Thr Leu	Gln Leu Ile Lys	Val Gln Glu
275	280	285	
Gly Val Gly Glu	Gly Lys Val Met Phe	His Ser Phe Val	Ser Lys Thr
290	295	300	
Glu Glu Glu Leu	Gln Ala Ile Leu Glu	Ala Lys Glu Lys	Lys Leu Arg
305	310	315	320
Leu Lys Ala Gln	Arg Gln Ala Gln Gln	Ala Gln Asn Val	Gln Arg Lys
325	330	335	
Gln Glu Gln Arg	Glu Ala His Arg Lys	Lys Ser Leu Glu	Gly Met Lys
340	345	350	
Lys Ala Arg Val	Gly Gly Ser Asp Glu	Glu Ala Ser Gly	Ile Pro Ser
355	360	365	
Arg Thr Ala Ser	Leu Glu Leu Gly Glu	Asp Asp His Glu	Gln Glu Asp
370	375	380	
Asp Asp Ile Glu	Tyr Phe Cys Gln Ala	Val Gly Glu Ala	Pro Ser Glu
385	390	395	400
Asp Leu Phe Pro	Glu Ala Lys Gln Lys	Arg Leu Ala Lys	Ser Pro Gly
405	410	415	
Arg Lys Arg Lys	Arg Trp Glu Met Asp	Arg Gly Arg Gly	Arg Leu Cys
420	425	430	

Asp Gln Lys Phe Pro Lys Thr Lys Asp Lys Ser Gln Gly Ala Gln Ala
435 440 445
Arg Arg Gly Pro Arg Gly Ala Ser Arg Asp Gly Gly Arg Gly Arg Gly
450 455 460
Arg Gly Arg Pro Gly Lys Arg Val Ala
465 470

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nnnnnggatc ctgtttccgc ccggttt 87

<210> 8
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
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<400> 8
gtccgtggta tattacctgg ta 22

<210> 9
<211> 20
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<400> 9
cgaaaccggg cggaacagg 20

<210> 10
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<212> RNA
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<220>
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<221> misc_feature
<222> (1)...(52)
<223> n = A,T,C or G

<400> 10
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<210> 11
<211> 27
<212> DNA
<213> homo sapien

<400> 11
ccatcctaatac gactcact atagggc 27

<210> 12
<211> 43
<212> DNA
<213> homo sapien

<220>
<221> misc_feature
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<400> 12
cgatgctcct ctgactcga gggtagacc tccccgacnc cct 43

<210> 13
<211> 38
<212> DNA
<213> Artificial Sequence

<220>
<223> primer

<400> 13
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<400> 14
cggctcaccg agatcgccc 20

<210> 15
<211> 21
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<220>

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<400> 15

ggccacgcgt cgactagtac t

21

<210> 16

<211> 429

<212> PRT

<213> mus musculus

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			20					25					30			
Val	Phe	Thr	Arg	Gly	Arg	Ala	Gly	Arg	Asn	Val	Arg	Gln	Leu	Ser	Leu	
		35					40					45				
Asp	Val	Arg	Arg	Val	Met	Glu	Pro	Leu	Thr	Ala	Thr	Arg	Leu	Gln	Val	
	50					55					60					
Arg	Lys	Lys	Asn	Ser	Leu	Lys	Asp	Cys	Val	Ala	Val	Ala	Gly	Pro	Leu	
65					70					75					80	
Gly	Val	Thr	His	Phe	Leu	Ile	Leu	Thr	Lys	Thr	Cys	Asn	Ser	Val	Tyr	
				85					90					95		
Leu	Lys	Leu	Met	Arg	Leu	Pro	Gly	Gly	Pro	Thr	Leu	Thr	Phe	Gln	Ile	
			100					105					110			
Ser	Lys	Tyr	Thr	Leu	Ile	Arg	Asp	Val	Val	Ser	Ser	Leu	Arg	Arg	His	
		115					120					125				
Arg	Met	His	Glu	Gln	Gln	Pro	Asn	His	Pro	Pro	Leu	Leu	Val	Leu	Asn	
	130					135					140					
Ser	Phe	Gly	Pro	Gln	Ala	Met	His	Ile	Lys	Leu	Met	Ala	Thr	Met	Phe	
145					150					155					160	
Gln	Asn	Leu	Phe	Pro	Ser	Ile	Asn	Val	His	Thr	Val	Asn	Leu	Asn	Thr	
				165					170					175		
Ile	Lys	Arg	Cys	Leu	Leu	Ile	Asn	Tyr	Asn	Pro	Asp	Ser	Cys	Glu	Leu	
			180					185					190			
Asp	Phe	Arg	His	Tyr	Ser	Val	Lys	Val	Val	Pro	Val	Gly	Ala	Ser	Arg	
		195					200					205				
Gly	Met	Lys	Lys	Leu	Leu	Gln	Glu	Lys	Phe	Pro	Asn	Met	Ser	Arg	Leu	
	210					215					220					
Gln	Asp	Ile	Ser	Glu	Leu	Leu	Ala	Thr	Gln	Val	Gly	Leu	Ser	Asp	Ser	
225					230					235					240	
Glu	Val	Glu	Pro	Asp	Gln	Glu	His	Asn	Ile	Thr	Glu	Leu	Pro	Gln	Ala	
				245					250					255		
Val	Ala	Gly	Arg	Gly	Asn	Met	Gln	Ala	Gln	Gln	Ser	Ala	Val	Arg	Leu	
		260						265					270			
Thr	Glu	Ile	Gly	Pro	Arg	Met	Thr	Leu	Gln	Leu	Ile	Lys	Ile	Gln	Glu	
		275					280					285				
Gly	Val	Gly	Glu	Gly	Asn	Val	Leu	Phe	His	Ser	Phe	Val	His	Lys	Thr	
	290					295					300					
Glu	Glu	Glu	Leu	Gln	Ala	Ile	Leu	Ala	Ala	Lys	Glu	Glu	Lys	Leu	Arg	
305					310					315					320	
Leu	Lys	Ala	Gln	Arg	Gln	Asn	Gln	Gln	Ala	Glu	Asn	Leu	Gln	Phe	Ser	
				325					330					335		

Arg Ser Cys Arg Gly Pro Gln Glu Glu Glu Pro Gly Arg His Lys Ala
 340 345 350
 Ser Pro Cys Lys Gly Arg Arg Glx Gln Glx Cys Glx Gly Pro Arg Gly
 355 360 365
 Thr Ala Arg Gly Gln Trp Gly Ala Gly Gln Pro Glu Asp Glu Glu Asp
 370 375 380
 Asp Ala Glu Tyr Phe Arg Gln Ala Val Gly Glu Glu Pro Asp Glu Asp
 385 390 395 400
 Leu Phe Pro Thr Ala Ala Lys Arg Arg Arg Gln Gly Gly Leu Leu Ala
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 Lys Lys Gln Arg Gly Phe Glu Gln Arg Pro Gly Asn Lys
 420 425

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 <211> 460
 <212> PRT
 <213> Drosophila

<400> 17

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 35 40 45
 Phe Arg Arg Ile Met Glu Pro Phe Thr Ala Ser Asn Leu Arg Glu Lys
 50 55 60
 Arg Met Asn Arg Ile Gln Asp Phe Val Cys Leu Ser Ser Phe Phe His
 65 70 75 80
 Val Ser His Met Gly Ile Phe Asn Lys Ala Ser Thr Gln Leu Ser Phe
 85 90 95
 Lys Val Val Arg Leu Pro Arg Gly Pro Ser Leu Thr Phe Lys Val His
 100 105 110
 Gln Phe Thr Leu Ala Arg Asp Val Ile Ser Leu Ser Lys Lys Gln Met
 115 120 125
 Ile Asp Asn Asp His Phe Lys His Ala Pro Leu Val Ile Met Asn Asn
 130 135 140
 Phe Ser Gly Asp Gly Lys His Leu Lys Leu Met Ala Thr Thr Phe Gln
 145 150 155 160
 Asn Met Phe Pro Ser Ile Asn Leu Ala Thr Val Asn Ile Gly Thr Ile
 165 170 175
 Arg Arg Cys Val Leu Phe Ser Tyr Asn Pro Asp Thr Lys Leu Val Glu
 180 185 190
 Met Pro His Tyr Ser Val Gln Val Val Pro Val Gly Leu Lys Arg Ala
 195 200 205
 Val Gln Lys Ile Val Lys Gly Thr Val Pro Asn Leu Gly Lys Cys Asn
 210 215 220
 Glu Val Val Asp Phe Val Thr Lys Asp Gly Tyr Ala Ser Glu Ser Glu
 225 230 235 240
 Ala Glu Asp Asp Glu Gln Ser His Val Val Leu Ala Gln Thr Leu Lys
 245 250 255
 Ser Lys Gly Asn Leu Glu Asp Lys Lys Ser Ser Ile Lys Leu His Glu
 260 265 270

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Ile Gly Pro Arg Leu Thr Met Gln Leu Ile Lys Ile Glu Glu Gly Leu
      275                280                285
Leu Thr Gly Glu Val Ile Tyr His Asp His Val Val Lys Thr Glu Asp
      290                295                300
Glu Lys Glu Thr Leu Arg Lys Leu Val Glu Lys Lys Arg Lys Gln Lys
305                310                315                320
Glu Gln Arg Lys Lys Glu Gln Ala Glu Asn Arg Ala Arg Asn Leu Lys
      325                330                335
Leu Lys Lys Asp Glu Lys Trp Ala Ala Lys Arg Ala Ala Glu Gly Arg
      340                345                350
Thr Asp Ser Asp Pro Glu Asp Asp Ala Glu Tyr Tyr Lys Glu Glu Val
      355                360                365
Gly Glu Glu Pro Asp Glu Glu Leu Phe Lys Met Glu Ala Lys Ser Ser
      370                375                380
Arg Lys Arg Pro Ser Leu Gly Gly Gly Met Lys Tyr Lys Asn Lys Arg
385                390                395                400
Ala Lys Leu Asp Thr Lys Asp Lys Asn Asp Lys Ser Glu Arg Thr Asp
      405                410                415
Lys Tyr Asp Arg Lys Asp Lys Phe Asp Arg Lys Asp Lys Lys Asp Lys
      420                425                430
Phe Asp Pro Lys Asn Gly Arg Ala Lys Phe Asp Pro Lys Asn Lys Arg
      435                440                445
Ala Lys Phe Asp His Arg Lys Ser Arg Lys Ser Lys
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 <211> 15
 <212> DNA
 <213> homo sapien

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15

<210> 19
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 <212> PRT
 <213> mus musulus

<220>
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Tyr Ala Ala Gln Pro His Ser Phe Val Phe Thr Arg Gly Arg Ala Gly
      35                40                45
Arg Asn Val Arg Gln Leu Ser Leu Asp Val Arg Arg Val Met Glu Pro
      50                55                60
Leu Thr Ala Thr Arg Leu Gln Val Arg Lys Lys Asn Ser Leu Lys Asp

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65				70					75				80		
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				85					90					95	
Thr	Lys	Thr	Asp	Asn	Ser	Val	Tyr	Leu	Lys	Leu	Met	Arg	Leu	Pro	Gly
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Gly	Pro	Thr	Leu	Thr	Phe	Gln	Ile	Ser	Lys	Tyr	Thr	Leu	Ile	Arg	Asp
		115					120					125			
Val	Val	Ser	Ser	Leu	Arg	Arg	His	Arg	Met	His	Glu	Gln	Gln	Phe	Asn
	130					135					140				
His	Pro	Pro	Leu	Leu	Val	Leu	Asn	Ser	Phe	Gly	Pro	Gln	Gly	Met	Lys
145					150					155					160
Ile	Lys	Leu	Met	Ala	Thr	Met	Phe	Gln	Asn	Leu	Phe	Pro	Ser	Ile	Asn
			165					170						175	
Val	His	Thr	Val	Asn	Leu	Asn	Thr	Ile	Lys	Arg	Cys	Leu	Leu	Ile	Asn
			180					185					190		
Tyr	Asn	Pro	Asp	Ser	Gln	Glu	Leu	Asp	Phe	Arg	His	Tyr	Ser	Val	Lys
		195					200					205			
Val	Val	Pro	Val	Gly	Ala	Ser	Arg	Gly	Met	Lys	Lys	Leu	Leu	Gln	Glu
	210					215					220				
Lys	Phe	Pro	Asn	Met	Ser	Arg	Leu	Gln	Asp	Ile	Ser	Glu	Leu	Leu	Ala
225					230					235					240
Thr	Gly	Val	Gly	Leu	Ser	Asp	Ser	Glu	Val	Glu	Pro	Asp	Gly	Glu	His
			245					250						255	
Asn	Thr	Thr	Glu	Leu	Pro	Gln	Ala	Val	Ala	Gly	Arg	Gly	Asn	Met	Gln
			260					265					270		
Ala	Gln	Gln	Ser	Ala	Val	Arg	Leu	Thr	Glu	Ile	Gly	Pro	Arg	Met	Thr
		275					280					285			
Leu	Gln	Leu	Ile	Lys	Ile	Gln	Glu	Gly	Val	Gly	Asn	Gly	Asn	Val	Leu
	290					295					300				
Phe	His	Ser	Phe	Val	His	Lys	Thr	Glu	Glu	Glu	Leu	Gln	Ala	Ile	Leu
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Ala	Ala	Lys	Glu	Glu	Lys	Leu	Arg	Leu	Lys	Ala	Gln	Arg	Gln	Asn	Gln
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Gln	Ala	Glu	Asn	Leu	Gln	Arg	Xaa	Arg	Ser	Cys	Arg	Xaa	Pro	Thr	Arg
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<210> 20
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Asn	Val	Tyr	Phe	Lys	Leu	Met	Arg	Leu	Pro	Gly	Gly	Pro	Thr	Leu	Thr
			20					25					30		

